

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/563,503A
Source: IFW
Date Processed by STIC: 6/14/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/563, 503A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 J Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
 Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/563,503A

DATE: 06/14/2006
TIME: 09:50:11

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06142006\J563503A.raw

*see item 2
on Euro summary
sheet*

5 <110> APPLICANT: Stordeur, Patrick
6 Goldman, Michel
10 <120> TITLE OF INVENTION: Device, kit and method for pulsing biological samples with
an agent and

11 stabilising the sample so pulsed
15 <130> FILE REFERENCE: DECLE35.005APC
19 <140> CURRENT APPLICATION NUMBER: 10/563,503A
20 <141> CURRENT FILING DATE: 2006-01-04
22 <150> PRIOR APPLICATION NUMBER: PCT/EP03/07453
23 <151> PRIOR FILING DATE: 2003-07-10
26 <160> NUMBER OF SEQ ID NOS: 10

28 <170> SOFTWARE: PatentIn version 3.1

32 <210> SEQ ID NO: 1

34 <211> LENGTH: 22

36 <212> TYPE: DNA

38 <213> ORGANISM: Homo sapiens

42 <400> SEQUENCE: 1

43 ctcaccagga tgctcacatt ta

44 <210> SEQ ID NO: 2

46 <211> LENGTH: 24

48 <212> TYPE: DNA

50 <213> ORGANISM: Homo sapiens

54 <400> SEQUENCE: 2

55 tccagagggtt tgagttcttc ttct

56 <210> SEQ ID NO: 3

58 <211> LENGTH: 25

60 <212> TYPE: DNA

62 <213> ORGANISM: Homo sapiens

66 <220> FEATURE:

68 <221> NAME/KEY: misc_feature

70 <222> LOCATION: (1)..(1)

72 <223> OTHER INFORMATION: N = 6Fam

75 <220> FEATURE:

77 <221> NAME/KEY: misc_feature

79 <222> LOCATION: (25)..(25)

81 <223> OTHER INFORMATION: N = Tamra-p

84 <400> SEQUENCE: 3

W--> 85 ntgccaaga aggccacaga actgn

86 <210> SEQ ID NO: 4

88 <211> LENGTH: 21

90 <212> TYPE: DNA

92 <213> ORGANISM: Homo sapiens

96 <400> SEQUENCE: 4

97 actttgaaca gcctcacaga g

**Does Not Comply
Corrected Diskette Needed**

pp 1-2

22

24

25

21

*h can only represent a nucleotide,
not a label or
dye.*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/563,503A

DATE: 06/14/2006
TIME: 09:50:11

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06142006\J563503A.raw

98 <210> SEQ ID NO: 5
100 <211> LENGTH: 20
102 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
108 <400> SEQUENCE: 5
109 ttggaggcag caaagatgtc 20
110 <210> SEQ ID NO: 6
112 <211> LENGTH: 23
114 <212> TYPE: DNA
116 <213> ORGANISM: Homo sapiens
120 <220> FEATURE:
122 <221> NAME/KEY: misc_feature
124 <222> LOCATION: (1)..(1)
126 <223> OTHER INFORMATION: N - 6Fam
129 <220> FEATURE:
131 <221> NAME/KEY: misc_feature
133 <222> LOCATION: (23)..(23)
135 <223> OTHER INFORMATION: N = Tamra-p
138 <400> SEQUENCE: 6
W--> 139 nctgtgcacc gagttgaccg tan 23
140 <210> SEQ ID NO: 7
142 <211> LENGTH: 22
144 <212> TYPE: DNA
146 <213> ORGANISM: Homo sapiens
150 <400> SEQUENCE: 7
151 tgtcacaaac agtgcaccta ct 22
152 <210> SEQ ID NO: 8
154 <211> LENGTH: 26
156 <212> TYPE: DNA
158 <213> ORGANISM: Homo sapiens
162 <400> SEQUENCE: 8
163 agttacaata ggtagcaaac cataca 26
164 <210> SEQ ID NO: 9
166 <211> LENGTH: 21
168 <212> TYPE: DNA
170 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 9
175 taattgcctc acattgtcac t 21
176 <210> SEQ ID NO: 10
178 <211> LENGTH: 21
180 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 10
187 attcagctcg aacactttga a 21

*Same env
as p.1*

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/563,503A

DATE: 06/14/2006
TIME: 09:50:12

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06142006\J563503A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1,25

Seq#:6; N Pos. 1,23

VERIFICATION SUMMARY

DATE: 06/14/2006

PATENT APPLICATION: US/10/563,503A

TIME: 09:50:12

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06142006\J563503A.raw

L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0



PAGE: 1
06/06/2006

VERIFICATION SUMMARY REPORT
PATENT APPLICATION

DATE:
TIME:

15:27:11

INPUT SEQ: A:\seq 1st-US.txt

GENERAL INFORMATION SECTION

5,<110> Stordeur, Patrick
6, Goldman, Michel
10,<120> Device, kit and method for pulsing biological
samples with an agent and stabilising the sample so pulsed
14,<130> DECLE35.005APC
18,<140> 10/563,503
19,<141> 2006-01-04
21,<150> PCT/EP03/07453
22,<151> 2003-07-10
25,<160> 10
27,<170> PatentIn version 3.1

ERRORED LINES SECTION

W--> 84 ntgcccaaga aggccacaga actgn
25
W--> 138 nctgtgcacc gagttgaccg tan
23

STATISTICS SUMMARY

Application Serial Number: 10/563,503
Alpha or Numeric or Xml: Numeric
Application Class:
Application File Date: 2006-01-04
Art Unit:
Software Application: PatentIN3.1
Total Number of Sequences: 10
Total Nucleotides: 225
Total Amino Acids: 0
Number of Errors: 0
Number of Warnings: 2
Number of Corrections: 0